SCORE Search Results Details for Application 10591347 and Search Result 20110118_143719_us-10-591-347-2_copy_1567_2124.rng.

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This page gives you Search Results detail for the Application 10591347 and Search Result 20110118_143719_us-10-591-347-2_copy_1567_2124.rng.

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                          GenCore version 6.3
                    Copyright (c) 1993 - 2011  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         January 18, 2011, 23:34:55 ; Search time 1207 Seconds
                                           (without alignments)
                                           9808.281 Million cell updates/sec

Title:          US-10-591-347-2_COPY_1567_2124
Perfect score:  558
Sequence:       1 agagacaatgaattaaggga.........atttgaagcacctgaatagg 558

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       18225500 seqs, 10608060480 residues

Total number of hits satisfying chosen parameters:      36451000

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        N_Geneseq_201023:*
                 1:  geneseqn1:*
                 2:  geneseqn2:*
                 3:  geneseqn3:*
                 4:  geneseqn4:*
                 5:  geneseqn5:*
                 6:  geneseqn6:*
                 7:  geneseqn7:*
```

8: geneseqn8:*
9: geneseqn9:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	558	100.0	3207	2	ADH68168	Adh68168 DNA encod
2	558	100.0	3207	4	AEF64785	Aef64785 Human pho
3	558	100.0	3207	4	AEK13515	Aek13515 Phosphati
4	558	100.0	3207	4	AEK13519	Aek13519 Phosphati
5	558	100.0	3207	7	ARL60529	Arl60529 Human pho
6	558	100.0	3412	1	AAQ51156	Aaq51156 Human p11
7	558	100.0	3412	4	AED31617	Aed31617 cDNA (SEQ
8	558	100.0	3423	3	ADU05935	Adu05935 Novel bro
9	558	100.0	3424	1	AAS14365	Aas14365 cDNA enco
10	558	100.0	3424	1	ABL59523	Abl59523 Human pho
11	558	100.0	3424	2	ADE85076	Ade85076 Farnesyl
12	558	100.0	3424	4	ADZ00490	Adz00490 p110-beta
13	558	100.0	3424	4	AEH10445	Aeh10445 PIK3CA cD
14	558	100.0	3424	4	AED31618	Aed31618 cDNA (SEQ
15	558	100.0	3424	4	AEG93388	Aeg93388 Human tum
16	558	100.0	3426	6	ARC02473	Arc02473 DNA fragm
17	558	100.0	3724	4	AEK54940	Aek54940 Human PIK
18	558	100.0	3724	5	AER29796	Aer29796 Breast ca
19	558	100.0	3724	7	ARV60468	Arv60468 Human PIK
20	558	100.0	3724	7	ARW65283	Arw65283 Human PIK
21	558	100.0	3724	7	ATM52123	Atm52123 Human PIK
22	558	100.0	3724	7	ATS16021	Ats16021 Human pho
23	558	100.0	3724	8	AWY98731	Awy98731 Human PIK
24	558	100.0	3724	8	AWY98891	Awy98891 Human PIK
25	558	100.0	3724	8	AWY98894	Awy98894 Human PIK
26	558	100.0	3724	9	AXU25358	Axu25358 Human pho
27	558	100.0	3724	9	AYE41305	Aye41305 Human PIK
28	558	100.0	7923	8	AWO77361	Awo77361 Expressio
29	556.4	99.7	3207	4	AEK13514	Aek13514 Phosphati
30	553.2	99.1	4326	8	AWY98838	Awy98838 Human PIK
31	533.8	95.7	3210	4	AEK13511	Aek13511 Phosphati
32	508.4	91.1	3207	1	AAQ51155	Aaq51155 p110 cDNA
33	508.4	91.1	3498	1	AAQ57012	Aaq57012 PtdIns 3-
34	457.8	82.0	3207	8	AWY98836	Awy98836 Human PIK
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36	271.6	48.7	459	1	AFS99247	Afs99247 Human tra
37	205	36.7	2397	1	AFS82080	Afs82080 Human tra
38	191.8	34.4	412	2	ABX37274	Abx37274 Bovine ES
39	144.8	25.9	3213	1	AAC65690	Aac65690 Human PI3
40	144.8	25.9	3213	1	AAS14366	Aas14366 cDNA enco
41	144.8	25.9	3213	1	ABV78026	Abv78026 Hypoxia-r
42	144.8	25.9	3213	1	AFS81712	Afs81712 Human tra

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ALIGNMENTS

RESULT 1
ADH68168
ID ADH68168 standard; DNA; 3207 BP.
XX
AC ADH68168;
XX
DT 25-MAR-2004 (first entry)
XX
DE DNA encoding a PI3K-alpha protein.
XX
KW G protein-coupled receptor; GPCR; phosphoinositide 3-kinase; PI3K; HEAT;
KW Beta-adrenergic receptor kinase 1; Beta-ARK1; cardiant; antiasthmatic;
KW nephrotropic; hypotensive; antianginal; antiarrhythmic;
KW antiarteriosclerotic; antiinflammatory; antidiabetic; antiallergic;
KW antirheumatic; antiarthritic; antiulcer; cardiant; ophthalmological;
KW analgesic; anorectic; antidepressant; tranquilizer; neuroprotective;
KW antiparkinsonian; nootropic; virucide; cytostatic; gene; ds.
XX
OS Homo sapiens.
XX
PN US2003182669-A1.
XX
PD 25-SEP-2003.
XX
PF 19-MAR-2002; 2002US-00101235.
XX
PR 19-MAR-2002; 2002US-00101235.
XX
PA (ROCK/) ROCKMAN H A.
PA (PRAS/) NAGA PRASAD S V.
PA (LAPO/) LAPORTE S A.
PA (BARA/) BARAK L S.
PA (CARO/) CARON M G.
XX
PI Rockman HA, Naga Prasad SV, Laporte SA, Barak LS, Caron MG;
XX
DR WPI; 2004-141485/14.
DR P-PSDB; ADH68169.
XX
PT Screening compounds useful for the treatment of e.g. asthma and angina
PT pectoris involves exposing cell comprising labeled molecule to compounds

PT and comparing locations of labeled molecules in presence and absence of
PT the compound.
XX
PS Disclosure; SEQ ID NO 7; 71pp; English.
XX
CC The invention relates to a novel method for screening compound(s) for
CC modulating G protein-coupled receptor (GPCR) internalization. The
CC compounds of the invention include modified phosphoinositide 3-kinase
CC (PI3K), modified HEAT domain, and modified Beta-adrenergic receptor
CC kinase 1 (Beta-ARK1). The method involves: exposing a cell comprising
CC labelled molecule to the compound(s); identifying the location of the
CC molecule in the cell; comparing the location in the presence and absence
CC of the compound(s); and correlating difference between the locations. The
CC GPCR modulating compounds have the following activities: cardiant,
CC antiasthmatic, nephrotropic, hypotensive, antianginal, antiarrhythmic,
CC antiarteriosclerotic, antiinflammatory, antidiabetic, antiallergic,
CC antirheumatic, antiarthritic, antiulcer, cardiant, ophthalmological,
CC analgesic, anorectic, antidepressant, tranquilizer, neuroprotective,
CC antiparkinsonian, nootropic, virucide, and cytostatic. The compounds are
CC useful for preventing and treating disease associated with GPCR activity
CC and phosphoinositide 3-kinase (PI3K) activity e.g. cardiovascular
CC disease, heart failure, asthma, nephrogenic diabetes insipidus and
CC hypertension, angina pectoris, essential hypertension, myocardial
CC infarction, supraventricular and ventricular arrhythmia, atherosclerosis,
CC renal failure, chronic bronchitis, diabetes, respiratory indications e.g.
CC bronchospasm, emphysema, airway obstruction, upper respiratory
CC indications e.g. rhinitis, seasonal allergies, inflammatory disease,
CC rheumatoid arthritis, chronic inflammatory bowel disease, glaucoma,
CC gastrointestinal indications e.g. acid/peptic disorder, oesophagitis,
CC gastrointestinal hyper-secretion, peptic ulcer, pain, obesity, bulimia
CC nervosa, depression, obsessive compulsive disorder, organ malformation,
CC neurodegenerative disorder e.g. Parkinson's disease, Alzheimer's disease,
CC multiple sclerosis, Epstein-Barr infection and cancer. The modified
CC phosphoinositide 3-kinase compound effectively alters the ability of wild
CC -type PI3K to bind Beta-ARK-1. This polynucleotide sequence represents
CC the DNA encoding a PI3K-alpha protein of the invention
XX
SQ Sequence 3207 BP; 1042 A; 579 C; 674 G; 912 T; 0 U; 0 Other;

Query Match 100.0%; Score 558; DB 2; Length 3207;
Best Local Similarity 100.0%;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1555 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1614

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db       1615 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1674

Qy        121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1675 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1734

Qy        181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1735 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1794

Qy        241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1795 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 1854

Qy        301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1855 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1914

Qy        361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1915 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 1974

Qy        421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
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Db       1975 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 2034

Qy        481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2035 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 2094

Qy        541 TTGAAGCACCTGAATAGG 558
              ||||||||||||||||||
Db       2095 TTGAAGCACCTGAATAGG 2112
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RESULT 2
AEF64785
ID   AEF64785 standard; cDNA; 3207 BP.
XX
AC   AEF64785;
XX
DT   06-APR-2006 (first entry)
XX
DE   Human phosphoinositide 3-kinase (PI3K) alpha cDNA.
XX
KW   Screening; diagnostic; gene therapy; cardiovascular disease;
KW   cardiovascular-gen.; cardiac failure; cardiant; asthma; antiasthmatic;
KW   nephrogenic diabetes insipidus; nephrotropic; hypertension; hypotensive;
KW   ss; gene; phosphoinositide 3-kinase.

XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .3207
FT /*tag= a
FT /product= "Human phosphoinositide 3-kinase (PI3K) gamma
FT protein"
XX
PN US2006026702-A1.
XX
PD 02-FEB-2006.
XX
PF 30-JUL-2004; 2004US-00902137.
XX
PR 19-MAR-2002; 2002US-00101235.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Rockman HA, Naga PSV, Laporte SA, Barak LS, Caron MG;
XX
DR WPI; 2006-153699/16.
DR P-PSDB; AEF64786.
XX
PT Screening compound(s) for modulating GPCR internalization, useful for
PT treating cardiovascular disease, asthma, nephrogenic diabetes insipidus,
PT or hypertension, by providing a cell comprising molecules involved in
PT GPCR internalization.
XX
PS Disclosure; SEQ ID NO 7; 86pp; English.
XX
CC The present invention relates to methods for screening compounds and test
CC solutions for the activity of modulating G protein-coupled receptor
CC (GPCR) internalization. The method involves providing a cell comprising
CC molecules involved in GPCR internalization, where the molecules involved
CC in GPCR internalization comprise beta-adrenergic receptor kinase 1
CC (betaARK1), phosphoinositide 3-kinase (PI3K), GPCR, and arrestin and
CC where at least one of the molecules is detectably labeled. The invention
CC is useful for treating cardiovascular disease, heart failure, asthma,
CC nephrogenic diabetes insipidus and hypertension. The invention is also
CC useful in gene therapy and in diagnostic techniques such as immunoassay.
CC The present sequence is a human phosphoinositide 3-kinase (PI3K) alpha
CC cDNA.
XX
SQ Sequence 3207 BP; 1042 A; 579 C; 674 G; 912 T; 0 U; 0 Other;

Query Match 100.0%; Score 558; DB 4; Length 3207;
Best Local Similarity 100.0%;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1555 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1614

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1615 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1674

Qy        121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1675 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1734

Qy        181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1735 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1794

Qy        241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1795 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 1854

Qy        301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1855 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1914

Qy        361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
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Qy        421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
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Qy        481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
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Db       2035 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 2094

Qy        541 TTGAAGCACCTGAATAGG 558
              ||||||||||||||||||
Db       2095 TTGAAGCACCTGAATAGG 2112
```

RESULT 3
AEK13515
ID   AEK13515 standard; cDNA; 3207 BP.
XX
AC   AEK13515;
XX
DT   02-NOV-2006 (first entry)

XX
DE Phosphatidylinositol 3'-kinase (PI3K) H1047L cDNA SEQ ID NO 54.
XX
KW cytostatic; gene therapy; mutation; diagnosis; prostate tumor; andrology;
KW genitourinary disease; neoplasm; ovary tumor; endocrine disease;
KW genitourinary disease; gynecology and obstetrics; head & neck tumor;
KW bladder tumor; brain tumor; neurological disease; gastrointestinal tumor;
KW gastrointestinal disease; colon tumor; breast tumor; lung tumor;
KW respiratory disease; phosphatidylinositol 3'-kinase; PI3K; mutant; gene;
KW ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT /*tag= a
FT /product= "Phosphatidylinositol 3'-kinase (PI3K) H1047L"
XX
PN WO2006091899-A2.
XX
PD 31-AUG-2006.
XX
PF 23-FEB-2006; 2006WO-US006751.
XX
PR 24-FEB-2005; 2005US-0656263P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Freeman D, Juan T, Radinsky R;
XX
DR WPI; 2006-648484/67.
DR P-PSDB; AEK13478.
XX
PT New isolated epidermal growth factor receptor (EGFr) polypeptides, useful
PT for treating EGFr-related cancer, e.g. non-small cell lung carcinoma,
PT breast, colon, gastric, brain, bladder, head and neck, ovarian, and
PT prostate carcinomas.
XX
PS Example 1; SEQ ID NO 54; 292pp; English.
XX
CC The invention describes an isolated epidermal growth factor receptor
CC (EPGFr) polypeptide comprising at least one amino acid sequence having
CC 766-1211 amino acids (SEQ ID NO: 2, 3, 5, 6, 7, 8, 9, 10, 12, 13, 15, 16,
CC 17, 19, or 20), given in the specification. The isolated polypeptide,
CC polynucleotides, and methods are useful for treating an EGFr-related
CC cancer, e.g. non-small cell lung carcinoma, breast, colon, gastric,
CC brain, bladder, head and neck, ovarian, and prostate carcinomas. This
CC sequence enodes human Phosphatidylinositol 3'-kinase (PI3K) H1047L
CC mutant.

XX
SQ Sequence 3207 BP; 1042 A; 586 C; 670 G; 909 T; 0 U; 0 Other;

Query Match 100.0%; Score 558; DB 4; Length 3207;
Best Local Similarity 100.0%;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1555 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1614

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
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Db       1615 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1674

Qy        121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1675 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1734

Qy        181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1735 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1794

Qy        241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1855 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1914

Qy        361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1915 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 1974

Qy        421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
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Qy        481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
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Qy        541 TTGAAGCACCTGAATAGG 558
              ||||||||||||||||||
Db       2095 TTGAAGCACCTGAATAGG 2112
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RESULT 4

```
AEK13519
ID   AEK13519 standard; cDNA; 3207 BP.
XX
AC   AEK13519;
XX
DT   11-JUN-2007  (revised)
DT   02-NOV-2006  (first entry)
XX
DE   Phosphatidylinositol 3'-kinase (PI3K) cDNA SEQ ID NO 58.
XX
KW   cytostatic; gene therapy; mutation; diagnosis; prostate tumor; andrology;
KW   genitourinary disease; neoplasm; ovary tumor; endocrine disease;
KW   genitourinary disease; gynecology and obstetrics; head & neck tumor;
KW   bladder tumor; brain tumor; neurological disease; gastrointestinal tumor;
KW   gastrointestinal disease; colon tumor; breast tumor; lung tumor;
KW   respiratory disease; phosphatidylinositol 3'-kinase; PI3K; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "PI3K"
XX
PN   WO2006091899-A2.
XX
PD   31-AUG-2006.
XX
PF   23-FEB-2006; 2006WO-US006751.
XX
PR   24-FEB-2005; 2005US-0656263P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Freeman D,  Juan T,  Radinsky R;
XX
DR   WPI; 2006-648484/67.
DR   P-PSDB; AEK13475.
DR   PC:NCBI; gi1763625.
DR   PC_ENCPRO:NCBI; gi1763626.
XX
PT   New isolated epidermal growth factor receptor (EGFr) polypeptides, useful
PT   for treating EGFr-related cancer, e.g. non-small cell lung carcinoma,
PT   breast, colon, gastric, brain, bladder, head and neck, ovarian, and
PT   prostate carcinomas.
XX
PS   Example 1; SEQ ID NO 58; 292pp; English.
XX
CC   The invention describes an isolated epidermal growth factor receptor
```

CC (EPGFr) polypeptide comprising at least one amino acid sequence having
CC 766-1211 amino acids (SEQ ID NO: 2, 3, 5, 6, 7, 8, 9, 10, 12, 13, 15, 16,
CC 17, 19, or 20), given in the specification. The isolated polypeptide,
CC polynucleotides, and methods are useful for treating an EGFr-related
CC cancer, e.g. non-small cell lung carcinoma, breast, colon, gastric,
CC brain, bladder, head and neck, ovarian, and prostate carcinomas. This
CC sequence encodes wild type human Phosphatidylinositol 3'-kinase (PI3K).
CC
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 3207 BP; 1043 A; 586 C; 670 G; 908 T; 0 U; 0 Other;

Query Match 100.0%; Score 558; DB 4; Length 3207;
Best Local Similarity 100.0%;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1555 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1614

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1615 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1674

Qy        121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1675 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1734

Qy        181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1735 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1794

Qy        241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1795 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 1854

Qy        301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1855 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1914

Qy        361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1915 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 1974

Qy        421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1975 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 2034
```

```
Qy         481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2035 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 2094

Qy         541 TTGAAGCACCTGAATAGG 558
               ||||||||||||||||||
Db        2095 TTGAAGCACCTGAATAGG 2112
```

RESULT 5
ARL60529
ID   ARL60529 standard; DNA; 3207 BP.
XX
AC   ARL60529;
XX
DT   16-OCT-2008 (first entry)
XX
DE   Human phosphoinositide-3-kinase catalytic alpha (PIK3CA) DNA, SEQ ID 23.
XX
KW   anti-hiv; antibacterial; antibiotic; bacterial infection; cancer;
KW   chlamydia infection; cns-gen.; coding sequence; cystic fibrosis;
KW   cytostatic; diagnostic test; ds; enzyme inhibition;
KW   escherichia coli infection; haemophilus infection; immune deficiency;
KW   immunostimulant; legionella infection; leishmania infection; leukemia;
KW   lung infection; mycobacterium infection; neutropenia; pharmaceutical;
KW   prophylactic to disease; respiratory-gen.; salmonella infection;
KW   staphylococcus infection; therapeutic; PIK3CA;
KW   phosphoinositide-3-kinase catalytic alpha.
XX
OS   Homo sapiens.
XX
PN   WO2008026075-A2.
XX
PD   06-MAR-2008.
XX
PF   31-AUG-2007; 2007WO-IB003553.
XX
PR   31-AUG-2006; 2006GB-00017222.
XX
PA   (VEHE-) VER HET NEDERLANDS KANKER INST.
PA   (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Neefjes JJ, Overkleeft HS, Ottenhoff THM, Savage NDL, Tuin AW;
PI   Marsman M, Kuijl CP;
XX
DR   WPI; 2008-L13796/65.
DR   REFSEQ; NM_0062182.
XX

PT Use of protein kinase inhibitor for the manufacture of medicament for
PT treating intracellular bacterial infection in subject.
XX
PS Claim 14; SEQ ID NO 23; 238pp; English.
XX
CC The present invention relates to the use of protein kinase inhibitors for
CC the manufacture of medicament for treating intracellular bacterial
CC infections. The inhibitor can be an organic compound or its isomers,
CC salts, solvates, chemically protected forms, or pro-drugs; an inhibitor
CC of the protein kinases; a ribozyme or RNA1 molecule that targets mRNA
CC encoding the protein kinase; a polynucleotide encoding a ribozyme or RNAi
CC molecule; or an antisense polynucleotide that is complementary to a
CC polynucleotide sequence encoding the protein kinase or its variant or
CC fragment. The invention was carried out by: (i) screening kinase
CC inhibitors for an effect on intracellular growth of salmonella, (ii)
CC synthesis of H-89 variants, (iii) testing the effect of H-89 and H-89
CC variants on bacterial intracellular growth, (iv) identification of host
CC cell kinases involved in intracellular salmonella growth using an shRNAi
CC library, (v) testing kinases for inhibition by H-89 and H-89 variants,
CC (vi) testing H-89 variants for an inhibitory effect on multi-drug
CC resistant bacteria and their in vivo antibacterial effect, (vii) siRNA
CC screening of human kinome, (viii) testing of the PKB/Akt1 inhibitors for
CC bactericidal effect. The protein kinase inhibitors of the present
CC invention are used for the manufacture of medicament for treating
CC intracellular bacterial infection (chlamydia infection, escherichia coli
CC infection, haemophilus infection, legionella infection, leishmania
CC infection, mycobacterium infection, salmonella infection, staphylococcus
CC infection). The method of the invention can be used to target diseases or
CC conditions in which intracellular bacterial infection is implicated,
CC namely neutropenia, immunodeficiency, acquired immune deficiency
CC syndrome, leukemia, cancer patients treated with cytostatic agents, lung
CC infections associated with cystic fibrosis. The present sequence is the
CC coding sequence of human phosphoinositide-3-kinase catalytic alpha
CC polypeptide (PIK3CA), the inhibition of which inhibits intracellular
CC bacterial growth related to the invention.
XX
SQ Sequence 3207 BP; 1043 A; 584 C; 669 G; 911 T; 0 U; 0 Other;

Query Match 100.0%; Score 558; DB 7; Length 3207;
Best Local Similarity 100.0%;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1555 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1614

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1615 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1674
```

```
Qy         121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1675 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1734

Qy         181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1735 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1794

Qy         241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1795 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 1854

Qy         301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1855 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1914

Qy         361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1915 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 1974

Qy         421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1975 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 2034

Qy         481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2035 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 2094

Qy         541 TTGAAGCACCTGAATAGG 558
               ||||||||||||||||||
Db        2095 TTGAAGCACCTGAATAGG 2112
```

RESULT 6
AAQ51156
ID   AAQ51156 standard; cDNA; 3412 BP.
XX
AC   AAQ51156;
XX
DT   25-MAR-2003 (revised)
DT   12-APR-1994 (first entry)
XX
DE   Human p110 cDNA.
XX
KW   Phosphoinositide kinase; PI; p85 subunit; screening; agonist; antagonist;
KW   cell proliferation; inhibition; prophylaxis; therapy; platelets;
KW   neutorphil activity; 3-phosphorylated phosphoinositides; ds.
XX

```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3207
FT                   /*tag=  a
FT                   /note= "PI3- kinase p110"
XX
PN   WO9321328-A1.
XX
PD   28-OCT-1993.
XX
PF   13-APR-1993;   93WO-GB000761.
XX
PR   13-APR-1992;   92GB-00008135.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Hiles ID,  Fry MJ,  Dhand R,  Waterfield MD,  Parker PJ,  Otsu M;
PI   Panayotou G,  Volinia S,  Gout I;
XX
DR   WPI; 1993-351738/44.
DR   P-PSDB; AAR43342.
XX
PT   Recombinant polypeptide(s) - with phosphoinositide-3 kinase activity,
PT   useful for controlling cell proliferation.
XX
PS   Claim 7; Fig 16; 146pp; English.
XX
CC   Southern blot analysis was performed using a bovine cDNA probe contg. a
CC   fragment of a PI3-kinase-encoding sequence and human cDNA isolated from a
CC   cDNA library constructed from mRNA isolated from the human cell line
CC   KG1a. Positive clones were sequenced to give the human PI3 kinase p110
CC   sequence shown. This sequence has 95 percent homology with the bovine
CC   sequence. The domain encoding residues 19- 100 of human p110 is
CC   sufficient to encode the kinase which will associate with the p85 kinase
CC   subunit. The gene may be used to provide a protein with PI3 kinase
CC   activity, and is useful for screening for (ant)agonists of PI3 kinase
CC   activity which could be useful for stimulation or inhibition of cell
CC   proliferation and hence prophylaxis or therapy. Platelet or neutrophil
CC   activity or blood glucose levels can be controlled using the kinase. See
CC   also AAQ51155 and AAQ57522-3. (Updated on 25-MAR-2003 to correct PN
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 3412 BP; 1128 A; 616 C; 706 G; 962 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 558;  DB 1;  Length 3412;
  Best Local Similarity   100.0%;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1555 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1614

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1615 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1674

Qy        121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1675 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1734

Qy        181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1735 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1794

Qy        241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1795 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 1854

Qy        301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1855 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1914

Qy        361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1915 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 1974

Qy        421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1975 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 2034

Qy        481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2035 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 2094

Qy        541 TTGAAGCACCTGAATAGG 558
              ||||||||||||||||||
Db       2095 TTGAAGCACCTGAATAGG 2112
```

RESULT 7
AED31617
ID   AED31617 standard; cDNA; 3412 BP.
XX
AC   AED31617;
XX
DT   15-DEC-2005 (first entry)
XX

DE cDNA (SEQ ID No:1) encoding human phosphatidylinositol 3-kinase (PIK3CA).
XX
KW cancer; neoplasm; phosphatidylinositol 3-kinase; PIK3CA; tumor;
KW chemotherapy; cytostatic; RNA interference; gene silencing;
KW antisense therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .3207
FT /*tag= a
FT /product= "PIK3CA"
XX
PN WO2005091849-A2.
XX
PD 06-OCT-2005.
XX
PF 18-FEB-2005; 2005WO-US005193.
XX
PR 02-MAR-2004; 2004US-0548886P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Samuels Y, Velculescu V, Kinzler KW, Vogelstein B;
XX
DR WPI; 2005-713721/73.
DR P-PSDB; AED31619.
XX
PT Assessing cancer in a human suspected of having cancer, by determining a
PT non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase
PT (PIK3CA) coding sequence in the body sample from a human.
XX
PS Disclosure; SEQ ID NO 1; 107pp; English.
XX
CC The invention relates to a method of assessing cancer in a body sample of
CC a human suspected of having cancer. The method comprises determining a
CC non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase
CC (PIK3CA) coding sequence in the body sample, and identifying the human as
CC likely to have cancer if a non-synonymous, intragenic mutation in PIK3CA
CC coding sequence is determined in the body sample. Also described are: (1)
CC a method of inhibiting progression of a tumor in a human; (2) a method of
CC identifying candidate chemotherapeutic agents; (3) a method for
CC delivering an appropriate chemotherapeutic drug to a patient in need; and
CC (4) a set of one or more primers for amplifying and/or sequencing PIK3CA,
CC the primers selected from forward primers, reverse primers, or sequencing
CC primers, where the forward primers are selected from sequences given as
CC SEQ ID NOs 6-165, the reverse primers are selected from sequences given
CC as SEQ ID NOs 166-325, and the sequencing primers are selected sequences
CC given as SEQ ID NOs 326-485 in the specification. The method of the

CC invention is useful for assessing cancer in a body sample of a human
CC suspected of having cancer, inhibiting progression of a tumor in a human,
CC identifying candidate chemotherapeutic agents, and delivering an
CC appropriate chemotherapeutic drug to a patient in need. This sequence
CC encodes human PIK3CA.
XX
SQ Sequence 3412 BP; 1128 A; 616 C; 706 G; 962 T; 0 U; 0 Other;

Query Match 100.0%; Score 558; DB 4; Length 3412;
Best Local Similarity 100.0%;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1555 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1614

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1615 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1674

Qy        121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1675 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1734

Qy        181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1735 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1794

Qy        241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1795 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 1854

Qy        301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1855 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1914

Qy        361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1915 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 1974

Qy        421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1975 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 2034

Qy        481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2035 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 2094

Qy        541 TTGAAGCACCTGAATAGG 558
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              ||||||||||||||||||
Db       2095 TTGAAGCACCTGAATAGG 2112


RESULT 8
ADU05935
ID   ADU05935 standard; DNA; 3423 BP.
XX
AC   ADU05935;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Novel bronchial cancer-associated human gene SeqID157.
XX
KW   bronchial cancer; cytostatic; tumour-associated protein;
KW   cancer detection; metastasis; tumour; gene; ds; human.
XX
OS   Homo sapiens.
XX
PN   DE10316701-A1.
XX
PD   04-NOV-2004.
XX
PF   09-APR-2003; 2003DE-01016701.
XX
PR   09-APR-2003; 2003DE-01016701.
XX
PA   (HINZ/) HINZMANN B.
PA   (HERM/) HERMANN K.
PA   (CAST/) HEIDEN CASTANOS-VELEZ E.
XX
PI   Mennerich D,  Bruemmendorf T,  Heiden E,  Hermann K,  Kinnemann H;
PI   Li X,  Roepcke S,  Staub E,  Hinzmann B,  Rosenthal A,  Pilarsky C;
XX
DR   WPI; 2004-786403/78.
DR   P-PSDB; ADU06422.
XX
PT   New nucleic acid, and derived proteins, useful for diagnosis of bronchial
PT   cancer and in screening for therapeutic and diagnostic agents.
XX
PS   Claim 1; SEQ ID NO 157; 1381pp; German.
XX
CC   This invention relates to a novel isolated nucleic acid associated with
CC   bronchial cancer comprising 489 defined sequences given in the
CC   specification. The invention may be useful for the production of
CC   compounds with a cytostatic activity through the inhibition of expression
CC   or activity of tumour-associated proteins. The novel DNA sequences and
CC   the proteins/peptides encoded by them are used for detecting bronchial
CC   cancer or determining the risk of developing it and to screen for
```

CC specific binding partners of the DNA or protein sequences, where the
CC binding partners are potentially useful as agents for treating or
CC diagnosing bronchial cancer. The DNA or protein sequences can also be
CC used for prognosis, detection of metastases and for secondary treatment
CC (of tumours that have been stabilised or are no longer detectable).
CC Detecting abnormal expression of the DNA sequences provides early
CC diagnosis of bronchial cancers. The present sequence is that of a novel
CC bronchial cancer-associated human gene sequence of the invention.
XX
SQ Sequence 3423 BP; 1134 A; 618 C; 709 G; 962 T; 0 U; 0 Other;

Query Match 100.0%; Score 558; DB 3; Length 3423;
Best Local Similarity 100.0%;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1567 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1626

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1627 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1686

Qy        121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1687 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1746

Qy        181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1747 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1806

Qy        241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1807 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 1866

Qy        301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1867 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1926

Qy        361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1927 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 1986

Qy        421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1987 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 2046

Qy        481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       2047 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 2106

Qy        541 TTGAAGCACCTGAATAGG 558
              ||||||||||||||||||
Db       2107 TTGAAGCACCTGAATAGG 2124


RESULT 9
AAS14365
ID   AAS14365 standard; cDNA; 3424 BP.
XX
AC   AAS14365;
XX
DT   11-JUN-2007  (revised)
DT   12-MAR-2002  (first entry)
XX
DE   cDNA encoding human p110alpha isoform of PI3-kinase.
XX
KW   Human; phosphatidylinositol 3-kinase; PI3K; p110alpha isoform; LASP-1;
KW   cancer; inflammatory disease; ophthalmic disorder; SH3 domain;
KW   autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
KW   Type I diabetes mellitus; cytostatic; immunosuppressive; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             13. .3219
FT                   /*tag=  a
FT                   /product= "p110alpha isoform of PI3-kinase"
XX
PN   WO200185986-A2.
XX
PD   15-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-US015065.
XX
PR   10-MAY-2000; 2000US-0203346P.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Sadhu C;
XX
DR   WPI; 2002-075252/10.
DR   P-PSDB; AAU09687.
DR   PC:NCBI; gi472990.
DR   PC_ENCPRO:NCBI; gi472991.
XX
PT   Identifying a modulator of p110delta polypeptide binding to SH3 domain-
PT   containing polypeptides e.g. LASP-1, comprising allowing the binding
```

PT partners to interact in the presence and absence of a test compound.
XX
PS Example 1; Page 55-60; 85pp; English.
XX
CC The present invention relates to identifying a modulator of the
CC phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to the
CC catalytic subunit via a SH3 domain-containing polypeptide such as LASP-1.
CC Also described are methods of assaying the specific binding affinity of
CC the PI3-kinase binding partner. Such modulators are useful for the
CC treatment of diseases characterised by the undesirable or excessive
CC activity of PI3Kdelta. For example the modulators can be used for
CC inhibiting the growth or proliferation of cancer cells (e.g. malignant
CC neoplasms of lymphoid and reticuloendothelial tissues, Hodgkin's
CC lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid arthritis),
CC ophthalmic disorders (e.g. allergic conjunctivitis), autoimmune diseases
CC (e.g. systematic lupus erythematosus), inflammatory bowel diseases (e.g.
CC chronic inflammatory bowel disease), inflammatory dermatoses (e.g.
CC contact dermatitis; central or peripheral nervous system inflammatory
CC disorders (e.g. meningitis), bacterial pneumonia, and Type I diabetes
CC mellitus. The present sequence encodes for human p110alpha isoform of
CC PI3k
CC
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 100.0%; Score 558; DB 1; Length 3424;
Best Local Similarity 100.0%;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1567 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1626

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1627 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1686

Qy        121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1687 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1746

Qy        181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1747 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1806

Qy        241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db       1807 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 1866

Qy        301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1867 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1926

Qy        361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1927 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 1986

Qy        421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1987 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 2046

Qy        481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2047 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 2106

Qy        541 TTGAAGCACCTGAATAGG 558
              ||||||||||||||||||
Db       2107 TTGAAGCACCTGAATAGG 2124
```

```
RESULT 10
ABL59523
ID   ABL59523 standard; cDNA; 3424 BP.
XX
AC   ABL59523;
XX
DT   11-JUN-2007  (revised)
DT   16-JUL-2002  (first entry)
XX
DE   Human phosphatidylinositol-3-kinase catalytic alpha cDNA SEQ ID NO:23.
XX
KW   Human; phosphatidylinositol-3-kinase catalytic alpha; enzyme; tumour;
KW   lipid associated gene; lipid metabolism; lipid synthesis;
KW   chromosome 3q26.3; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200227028-A1.
XX
PD   04-APR-2002.
XX
PF   27-SEP-2001; 2001WO-US030366.
XX
PR   28-SEP-2000; 2000US-00676052.
XX
PA   (ATAI-) ATAIRGIN TECHNOLOGIES INC.
```

XX
PI Skinner MK, Patton JL, Chaudhary J;
XX
DR WPI; 2002-405056/43.
DR PC:NCBI; gi472990.
DR PC_ENCPRO:NCBI; gi472991.
XX
PT Identifying tumor characteristics in a tissue sample taken from a
PT patient, involves determining the copy number or expression level of
PT genes associated with lipid metabolism, synthesis or action.
XX
PS Example 1; Page 82-83; 113pp; English.
XX
CC The present invention describes a method for identifying tumour
CC characteristics, comprising measuring a copy number or expression level
CC of at least two genes associated with lipid metabolism, synthesis, or
CC action in cells from a patient tissue sample, and comparing the results
CC with a copy number or expression level of the genes in a normal cell.
CC Also described is an array of nucleic acid polymers immobilised on a
CC solid support, comprising a solid support, at least two different nucleic
CC acid polymers which are each specific for a different gene associated
CC with lipid metabolism, synthesis or action, where each nucleic acid
CC polymer is located at a predetermined position on the solid support, and
CC the array comprises nucleic acid polymers which are specific for less
CC than 100 genes other than the selected genes. The method is useful for
CC determining tumour characteristics in a tissue sample taken from a
CC patient. The present sequence represents a human lipid-associated gene
CC related cDNA sequence, which is used in the exemplification of the
CC present invention
CC
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 100.0%; Score 558; DB 1; Length 3424;
Best Local Similarity 100.0%;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1567 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1626

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1627 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1686

Qy        121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db       1687 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1746

Qy        181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1747 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1806

Qy        241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1807 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 1866

Qy        301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1867 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1926

Qy        361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1927 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 1986

Qy        421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1987 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 2046

Qy        481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2047 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 2106

Qy        541 TTGAAGCACCTGAATAGG 558
              ||||||||||||||||||
Db       2107 TTGAAGCACCTGAATAGG 2124
```

```
RESULT 11
ADE85076
ID   ADE85076 standard; DNA; 3424 BP.
XX
AC   ADE85076;
XX
DT   11-JUN-2007  (revised)
DT   29-JAN-2004  (first entry)
XX
DE   Farnesyl transferase inhibitor modulated leukemia associated gene #295.
XX
KW   ss; cytostatic; farnesyl transferase inhibitor; gene expression;
KW   quinolinone; leukemia; cancer.
XX
OS   Homo sapiens.
XX
PN   WO2003038129-A2.
XX
```

PD 08-MAY-2003.
XX
PF 30-OCT-2002; 2002WO-US034784.
XX
PR 30-OCT-2001; 2001US-0338997P.
PR 30-OCT-2001; 2001US-0340081P.
PR 30-OCT-2001; 2001US-0340938P.
PR 30-OCT-2001; 2001US-0341012P.
XX
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI Raponi M;
XX
DR WPI; 2003-513497/48.
DR PC:NCBI; gi472990.
DR PC_ENCPRO:NCBI; gi472991.
XX
PT Determining whether a patient will respond to treatment with a farnesyl
PT transferase inhibitor, by analyzing the expression of gene that is
PT differentially modulated in the presence of the inhibitor.
XX
PS Disclosure; SEQ ID NO 295; 346pp; English.
XX
CC The invention relates to a method of determining whether a patient will
CC respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC analyzing the expression of gene that is differentially modulated in the
CC presence of an FTI. The method is useful for determining whether a
CC patient will respond to treatment with a FTI such as (B)-6-[amino(4-
CC chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-
CC methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a
CC patient with leukemia with FTI if the analysis indicates that the patient
CC will respond. This sequence corresponds to a gene whose expression may be
CC modulated in the presence of FTI.
CC
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 100.0%; Score 558; DB 2; Length 3424;
Best Local Similarity 100.0%;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1567 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1626

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db       1627 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1686

Qy        121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1687 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1746

Qy        181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1747 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1806

Qy        241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1807 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 1866

Qy        301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1867 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1926

Qy        361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1927 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 1986

Qy        421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1987 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 2046

Qy        481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2047 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 2106

Qy        541 TTGAAGCACCTGAATAGG 558
              ||||||||||||||||||
Db       2107 TTGAAGCACCTGAATAGG 2124
```

```
RESULT 12
ADZ00490
ID   ADZ00490 standard; cDNA; 3424 BP.
XX
AC   ADZ00490;
XX
DT   11-JUN-2007  (revised)
DT   16-JUN-2005  (first entry)
XX
DE   p110-beta coding sequence.
XX
KW   ss; Anorectic; Antidiabetic; p110-beta; phosphoinositide 3-kinase; p85;
KW   ras; insulin resistance; obesity; gene.
XX
```

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 13. .3219
FT /*tag= a
XX
PN WO2005031341-A2.
XX
PD 07-APR-2005.
XX
PF 28-SEP-2004; 2004WO-IB003926.
XX
PR 29-SEP-2003; 2003US-0507226P.
PR 13-JUL-2004; 2004US-0587333P.
XX
PA (PFIZ) PFIZER HEALTH AB.
XX
PI Bougneres P;
XX
DR WPI; 2005-273421/28.
DR P-PSDB; ADZ00491.
DR GENBANK; Z29090.
DR PC:NCBI; gi472990.
DR PC_ENCPRO:NCBI; gi472991.
XX
PT Predicting a subject's likelihood of developing insulin resistance,
PT useful for treating insulin resistance and obesity, comprises determining
PT in a subject the identity of an allele at position 100 of a specific
PT sequence.
XX
PS Disclosure; SEQ ID NO 2; 88pp; English.
XX
CC This sequence represents the p110-beta gene. p110-beta is a catalytic
CC subunit of a phosphoinositide 3-kinase, which also comprises a regulatory
CC subunit of about 85 kD. The p110 protein comprises a kinase domain at the
CC C-terminus, and a p85 and ras binding domain at the N-terminus. The
CC method of the invention for predicting a subject's likelihood of
CC developing insulin resistance comprises determining in a subject the
CC identity of the nucleotide present at a position corresponding to
CC position -359 of the p110-beta gene , where the allele comprising the
CC nucleotide is correlated with an increased or decreased likelihood of
CC developing insulin resistance. The method of the invention is useful for
CC treating obesity and insulin resistance and for assessing and conducting
CC clinical trials of medicaments.
CC
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 558;  DB 4;  Length 3424;
  Best Local Similarity   100.0%;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1567 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1626

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1627 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1686

Qy        121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1687 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1746

Qy        181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1747 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1806

Qy        241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1807 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 1866

Qy        301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1867 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1926

Qy        361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1927 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 1986

Qy        421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1987 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 2046

Qy        481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2047 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 2106

Qy        541 TTGAAGCACCTGAATAGG 558
              ||||||||||||||||||
Db       2107 TTGAAGCACCTGAATAGG 2124


RESULT 13
AEH10445
ID   AEH10445 standard; cDNA; 3424 BP.
```

XX
AC AEH10445;
XX
DT 11-JUN-2007 (revised)
DT 01-JUN-2006 (first entry)
XX
DE PIK3CA cDNA SEQ ID 831.
XX
KW gene expression; prognosis; diagnosis; DNA microarray;
KW colorectal disease; colon tumor; colorectal tumor; cytostatic;
KW gastrointestinal disease; neoplasm; ss.
XX
OS Unidentified.
XX
PN WO2005054508-A2.
XX
PD 16-JUN-2005.
XX
PF 01-DEC-2004; 2004WO-IB004323.
XX
PR 01-DEC-2003; 2003US-0525987P.
PR 01-DEC-2004; 2004US-00000688.
XX
PA (IPSO-) IPSOGEN.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (PAOL-) INST PAOLI CALMETTES IPC.
XX
PI Bertucci F, Houlgatte R, Birnbaum D, Debono S;
XX
DR WPI; 2005-435408/44.
DR PC:NCBI; gi472990.
XX
PT Analyzing differential gene expression associated with histopathologic
PT features of colorectal disease, involves detecting overexpression or
PT underexpression of pool of polynucleotide sequences in colon tissues.
XX
PS Claim 1; SEQ ID NO 831; 154pp; English.
XX
CC The invention describes a method of analyzing (M1) differential gene
CC expression associated with histopathologic features of colorectal
CC disease, comprising detecting overexpression or underexpression of a pool
CC of polynucleotide sequences in colon tissues, the pool selected in each
CC of predefined polynucleotide sequence sets chosen from any one of 644
CC sequence sets comprising combinations of SEQ ID No. 1-1596, fully defined
CC in the specification. Also described are: a polynucleotide library (I)
CC useful for the molecular characterization of a colon cancer, comprising
CC or corresponding to a pool of polynucleotide sequences either
CC overexpressed or underexpressed in colon tissue, the pool corresponding
CC to all or part of the polynucleotide sequence chosen from PS1; and

CC assigning (M2) a therapeutic regimen to patient with histopathological
CC features of colorectal disease, e.g. colon cancer, comprising classifying
CC the patient having a poor prognosis or a good prognosis on the basis of
CC (M1), assigning the patient a therapeutic regimen, the therapeutic
CC regiment comprising no adjuvant chemotherapy if the patient is lymph node
CC negative and is classified as having a good prognosis or comprising
CC chemotherapy if the patient has any other combination of lymph node
CC status and expression profile. (M1) is useful for analyzing differential
CC gene expression associated with histopathologic features of colorectal
CC disease. (M1) is useful for analyzing differential gene expression
CC associated with colon tumors, visceral metastases in colon cancer, lymph
CC node metastases in colon cancer, MSI phenotype in colon cancer, location
CC of primary colorectal carcinoma, in colon cancer, and survival and death
CC of patient in colon cancer, where the analysis comprises detection of
CC overexpression or underexpression of pool of polynucleotide sequences in
CC colon tissue, the pool corresponding to specific combination of
CC polynucleotide sequences from PS1, as given in the specification. (M1) is
CC useful for detecting, diagnosing, staging, classifying, monitoring or
CC predicting conditions associated with colorectal cancer. (M1) is useful
CC for prognosis or diagnosis or colon cancer or for monitoring the
CC treatment of a patient with colon cancer, which involves implementing
CC (M1) on nucleic acids from the patient. (M1) is useful for
CC differentiating a normal cell from a cancer cell, which involves
CC implementing (M1) on nucleic acids from the cells. (M1) is useful for
CC selecting appropriate doses and/or schedule of chemotherapeutics and/or
CC (bio)pharmaceuticals and/or target agents e.g. Irinotecan, 5-fluorouracil
CC and methotrexate. This sequence represents a polynucleotide identified in
CC the analysis of differential gene expression associated with
CC histopathological features of colorectal disease. Note: The sequence data
CC for this patent is not represented in the printed specification but is
CC based on sequence information supplied by the European Patent Office.
CC
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 100.0%; Score 558; DB 4; Length 3424;
Best Local Similarity 100.0%;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1567 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1626

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1627 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1686
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Qy         121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1687 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1746

Qy         181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1747 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1806

Qy         241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1807 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 1866

Qy         301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1867 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1926

Qy         361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1927 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 1986

Qy         421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1987 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 2046

Qy         481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2047 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 2106

Qy         541 TTGAAGCACCTGAATAGG 558
               ||||||||||||||||||
Db        2107 TTGAAGCACCTGAATAGG 2124
```

RESULT 14
AED31618
ID   AED31618 standard; cDNA; 3424 BP.
XX
AC   AED31618;
XX
DT   15-DEC-2005 (first entry)
XX
DE   cDNA (SEQ ID No:2) encoding human phosphatidylinositol 3-kinase (PIK3CA).
XX
KW   cancer; neoplasm; phosphatidylinositol 3-kinase; PIK3CA; tumor;
KW   chemotherapy; cytostatic; RNA interference; gene silencing;
KW   antisense therapy; gene; ss.
XX
OS   Homo sapiens.
XX

FH Key Location/Qualifiers
FT CDS 13. .3219
FT /*tag= a
FT /product= "PIK3CA"
XX
PN WO2005091849-A2.
XX
PD 06-OCT-2005.
XX
PF 18-FEB-2005; 2005WO-US005193.
XX
PR 02-MAR-2004; 2004US-0548886P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Samuels Y, Velculescu V, Kinzler KW, Vogelstein B;
XX
DR WPI; 2005-713721/73.
DR P-PSDB; AED31619.
XX
PT Assessing cancer in a human suspected of having cancer, by determining a
PT non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase
PT (PIK3CA) coding sequence in the body sample from a human.
XX
PS Claim 1; SEQ ID NO 2; 107pp; English.
XX
CC The invention relates to a method of assessing cancer in a body sample of
CC a human suspected of having cancer. The method comprises determining a
CC non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase
CC (PIK3CA) coding sequence in the body sample, and identifying the human as
CC likely to have cancer if a non-synonymous, intragenic mutation in PIK3CA
CC coding sequence is determined in the body sample. Also described are: (1)
CC a method of inhibiting progression of a tumor in a human; (2) a method of
CC identifying candidate chemotherapeutic agents; (3) a method for
CC delivering an appropriate chemotherapeutic drug to a patient in need; and
CC (4) a set of one or more primers for amplifying and/or sequencing PIK3CA,
CC the primers selected from forward primers, reverse primers, or sequencing
CC primers, where the forward primers are selected from sequences given as
CC SEQ ID NOs 6-165, the reverse primers are selected from sequences given
CC as SEQ ID NOs 166-325, and the sequencing primers are selected sequences
CC given as SEQ ID NOs 326-485 in the specification. The method of the
CC invention is useful for assessing cancer in a body sample of a human
CC suspected of having cancer, inhibiting progression of a tumor in a human,
CC identifying candidate chemotherapeutic agents, and delivering an
CC appropriate chemotherapeutic drug to a patient in need. This sequence
CC encodes human PIK3CA.
XX
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 558;  DB 4;  Length 3424;
  Best Local Similarity   100.0%;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1567 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1626

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1627 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1686

Qy        121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1687 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1746

Qy        181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1747 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1806

Qy        241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1807 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 1866

Qy        301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1867 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1926

Qy        361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1927 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 1986

Qy        421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1987 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 2046

Qy        481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2047 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 2106

Qy        541 TTGAAGCACCTGAATAGG 558
              ||||||||||||||||||
Db       2107 TTGAAGCACCTGAATAGG 2124


RESULT 15
AEG93388
ID   AEG93388 standard; cDNA; 3424 BP.
XX
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AC   AEG93388;
XX
DT   11-JUN-2007 (revised)
DT   01-JUN-2006 (first entry)
XX
DE   Human tumor cell cDNA SEQ ID NO:884.
XX
KW   Gene expression; tumor; ss.
XX
OS   Homo sapiens.
XX
PN   WO2006036025-A1.
XX
PD   06-APR-2006.
XX
PF   30-SEP-2005; 2005WO-JP018574.
XX
PR   30-SEP-2004; 2004JP-00286259.
PR   28-FEB-2005; 2005JP-00054475.
PR   28-FEB-2005; 2005JP-00054866.
XX
PA   (EISA) EISAI CO LTD.
XX
PI   Owa T, Yokoi A, Ozawa Y, Kawai T, Ushijima R;
XX
DR   WPI; 2006-293404/30.
DR   PC:NCBI; gi472990.
DR   PC_ENCPRO:NCBI; gi472991.
XX
PT   Evaluating sensitivity of a tumor cell to a sulfonamide-containing
PT   compound, comprises comparing the expression of specific genes in tumor
PT   cells before and after administration of the compound.
XX
PS   Claim 1; SEQ ID NO 884; 1405pp; Japanese.
XX
CC   The invention relates to a method of evaluating the sensitivity of a
CC   tumor cell to a sulfonamide-containing compound, by comparing the
CC   expression level of genes in tumor cells obtained from cancer patients
CC   before and after administration of the sulfonamide-containing compound
CC   and determining the tumor cell to be sensitive to the sulfonamide-
CC   containing compound, when the expression amount of genes in the cell is
CC   increased compared with the expression amount before administration
CC   and/or when the expression amount of one or more genes is decreased
CC   compared with the expression amount before administration. The invention
CC   also relates to an assay reagent of RNA comprising an oligonucleotide
CC   complementary to an RNA which is the transcription product of a gene, and
CC   an immunoassay reagent containing the antibody with respect to a protein
CC   which is a translation product of the gene. The expression level of the
CC   gene, which is the RNA transcription product, is measured using a DNA

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CC   microarray or by quantitative PCR. The expression level of protein, which
CC   is a translation product of the gene, is measured by an immunochemical
CC   method such as enzyme linked immunosorbent assay (ELISA),
CC   radioimmunoassay (RIA) or Western blotting. The method enables evaluation
CC   of the sensitivity of a tumor cell to a sulfonamide-containing compound.
CC   This sequence represents human tumor cell cDNA used in the scope of the
CC   invention.
CC
CC   Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 558;  DB 4;  Length 3424;
  Best Local Similarity   100.0%;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1567 AGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGAT 1626

Qy         61 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1627 CCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGT 1686

Qy        121 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1687 GTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGAT 1746

Qy        181 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1747 GAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCT 1806

Qy        241 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1807 ATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGC 1866

Qy        301 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1867 TTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTC 1926

Qy        361 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1927 CTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTG 1986

Qy        421 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 480
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Db       1987 ACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAA 2046
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Qy         481 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2047 ACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTAT 2106

Qy         541 TTGAAGCACCTGAATAGG 558
               ||||||||||||||||||
Db        2107 TTGAAGCACCTGAATAGG 2124
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Job time : 1540 secs